



hDEC2a

DEC1

MDEGIPHLQERQ—L——LEHRDFIGLDYSSLYMC-KPKRSMKRD-DTKDITYKLPHRLIEKKRRDRIN 61  
M-ERIPSAQPPPAKAPGLEHGDLPMPAHMYQVYKSRRGIKRSSESKETYKLPHRLIEKKRRDRIN 69

ECIAQLKOLLPEHLKLTTLGHLEKAVVLELTCLKHAKALTALTEQQHQKIIALQNG——ERSLKSPIQSD 127  
ECIAQLKOLLPEHLKLTTLGHLEKAVVLELTCLKHVKALTNLIDQQQKIIALQSGLQAGELSGR-NVETG 138

LDAFHSGFQTCAKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLTPQLLTQQVPLSKGTGA——PS 194  
QEMFCSGFQTCAREVLQYLAKHEN-T-RDLKSSQLVTHLHRVVSELLQGGTSRKPSDPAPKVMDFKEKPS 206

A-A-GSAAAPCLERAGQKLEPLAYCVPVIQRTQP-SAEAAENDTDTDSGYGGEAEARPD-R-E——K- 254  
SPAKGSEG-P——G-K--N——CVPVIQRTFAHSSGEQSGSDTDTDSGYGGESEKG-DLRSEQPCFKS 263

—GK—GAGASRVTIKQEPGEDSPAPK-RMKL-DSRGGG-SGGGPGGGAAAAAALLGPDPAALALR 317  
DHGRRFTMGERIGAIIKQESE-E-PPTKKNRMQLSDDEGHFTSS———D——— 305

PDAALLSSLVAFGGGGGAPFP-QAAAAAPFCLPFCFLSP-SAAAAVQPFLLDKSGLEKYLYPAAAAAPF 385  
——LISS—PFLG——PHPHQP——PFCLPF-YLIPPSATA-YL-PML——EKCWYPTSV—P- 349

PLLYPGIPAPAAAAAAAAAAAAAAAAAFPCLVSSVLPPEKAGAAAATLL-PHEVAPLGAPHPQHHPGRTH 454.  
VL-YPGLNASAAA———LSSFMNP—DKISA—PLLMPQR—L—PSP——— 385

LPFAGPREPGNPSSA—QE-DPSQPGK-EA-P 482  
LP-AHP——SVDSVLLQALKPIPLNLETKD

(Homology 43%)

FIG. 1



hDEC2a

hDEC2b

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTK--DTYKLPHRLIEKKRRDRINECIAQLK 68

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKVSDTYKLPHRLIEKKRRDRINECIAQLK 70

DLLPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKI IALQNGERSLKSPIQSDLD AFHSGFQTC 138

DLLPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKI IALQNGERSLKSPIQSDLD AFHSGFQTC 140

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 208

AKEVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSKGTGAPSAAGSAAAPCLERAG 210

QKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGGEAEARPDREKKGAGASRVTIKQEPPGEDSPAPK 278

QKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGGEAEARPDREKKGAGASRVTIKQEPPGEDSPAPK 280

RMKLDSRGGGSGGGPGGGAAAAAALLGPDPA AAAALLRPDAALLSSLVAFGGGGGAPFPQAAAAAPFC 348

RMKLDSRGGGSGGGPGGGAAAAAALLGPDPA AAAALLRPDAALLSSLVAFGGGGGAPFPQAAAAAPFC 350

LPFCFLSPSAAAAYVQPFLDKSGLEKYLPA AAAAPFLLYPGIPAPAAAAA AAAAAA AFPC LSSV 418

LPFCFLSPSAAAAYVQPFLDKSGLEKYLPA AAAAPFLLYPGIPAPAAAAA AAAAAA AFPC LSSV 420

LSPPPEKAGAAAATLLPHEVAPLGAPHPQH PHGRTHLPFAGPREPGNP ESSAQEDPSQPGKEAP 482

LSPPPEKAGAAAATLLPHEVAPLGAPHPQH PHGRTHLPFAGPREPGNP ESSAQEDPSQPGKEAP 484

FIG. 2

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hDEC2a  
mDEC2a

MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70  
MDEGIPHLQERQLLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALONGERSLKSPIQSOLD AFHSGFQTC AK 140  
LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALONGERSLKS PVQADL AFHSGFQTC AK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207  
EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTD TDSGYGGEAEARPDREKKGAGASRVTIKQEPPGEDS-P 275  
SGP-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A--V--KQEPPG-DSSP 249

APKRMKLDSRGGSGGGPGGGAAAAAALLGPDPA AAAALLRPDAALLSSLVAFGGGGGAPFPQAAAAA 345  
APKRPKLEARG-----ALLGPEPA---LL---G---SLVAL---GGGAPFAQPAAA--- 288

PFCLPFCFLSPSAAAAYVQPFLDKSGLEKYL PAAAAAPFLLYPGIPAPAAAAA AAAAAA AF PCL 415  
PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYLP AAAA-PFLLYPGIPA-----AAAAA AF PCL 348

SSVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQH PHGRTHLPFAGPREPGNP ESSAQEDPSQPGKEAP 482  
SSVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQH AHSRTHLPRAV-----NP ESS-QEDATQPAKDAP 410

FIG. 3



hDEC2a

mDEC2a

SHARP-1

MDEGIPHLQERQLEHRDFIGLDYSSLYMCKPKRSMKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

MDEGIPHLQERQLEHRDFIGLDYSSLYMCKPKRSLKRDDTKDITYKLPHRLIEKKRRDRINECIAQLKDL 70

LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPIQSDLD AFHSGFQTC AK 140

LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLD AFHSGFQTC AK 140

LPEHLKLTTLGHLEKAVVLELTCLKHLKALTALTEQQHQKIIALQNGERSLKSPVQADLD AFHSGFQTC AK 140

EVLQYLSRFESWTPREPRCVQLINHLHAVATQFLPTPQLLTQQVPLSK-GTG-AP-SAAGSAAAPCLERA 207

EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VP-SGRGSGRAPCSA-G-AAA-----A 196

EVLQYLARFESWTPREPRCAQLVSHLHAVATQLL-TPQ-----VT-PGRGPGRAPCSA-G-AAA-----A 196

-GQKLEPLAYCVPVIQRTQPSAELAAENDTDTDSGYGGEAEARPDREKKGAGASRVTIKQEPPGEDS-P 275

SGP-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A-V-KQEPPG-DSSP 249

SGS-ERVARCVPVIQRTQPGTEP-EHDTDTDSGYGGEAE-QG-R-----A-A-V-KQEPPG-DPSL 249

APKRMKLDSRGGGSGGGPGGGAAAAAALLGPDPAALLLRPDAALLSSLVAFGGGGGAPFPQAAAAA 345

APKRPKLEARG-----ALLGPEPA-LL-G-SLVAL-GGGAPFAQPAAL 288

RPRG

253

PFCLPFCFLSPSAAAAAYVQPFLDKSGLEKYLPAAPFLLYPGIPAPAAAAAFAFPCL 415

PFCLPFYLLSPSAAA-YVQPWLDKSGLDKYLPAAPFLLYPGIPA-----AAAAAFAFPCL 348

SSVLSPPPEKAGA-AAATLLPHEVAPLGAP-HPQHPHGRTHLPFAGPREPGNPRESSAQEDPSQPGKEAP 482

SSVLSPPPEKAGATAGAPFLAHEVAPPG-PLRPQHAHSRTHLPRAV-----NPRESS-QEDATQPAKDAP 410

FIG. 4